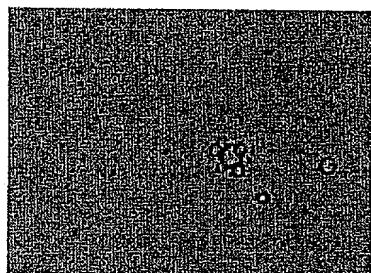
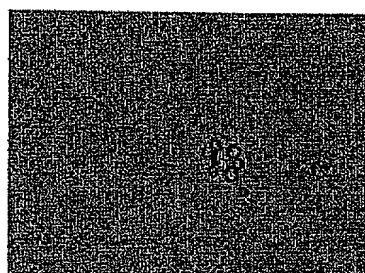


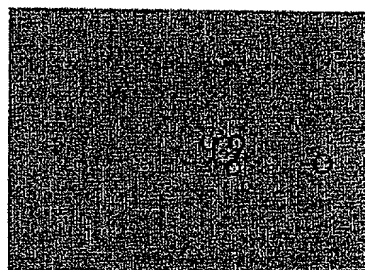
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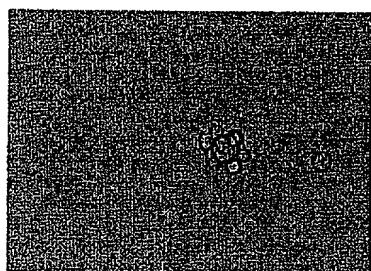
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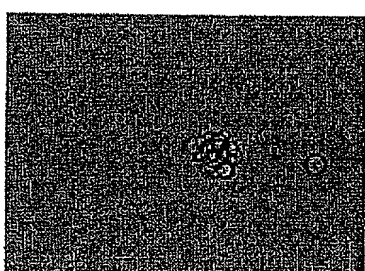
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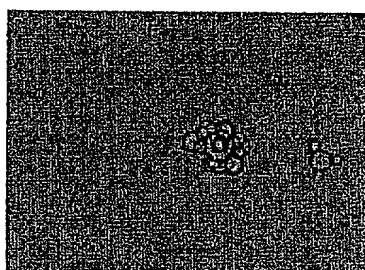
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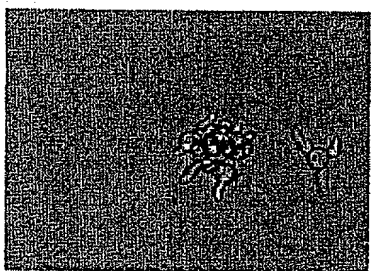
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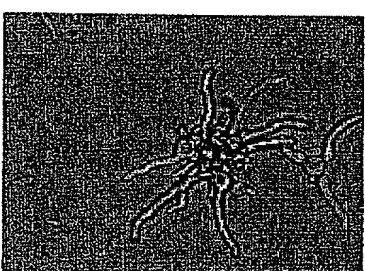
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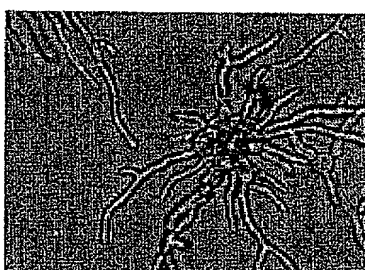
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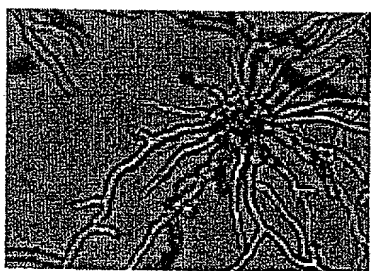
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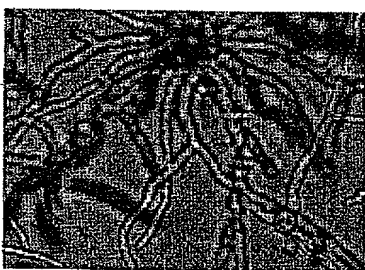
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9



10



11

Fig. 1

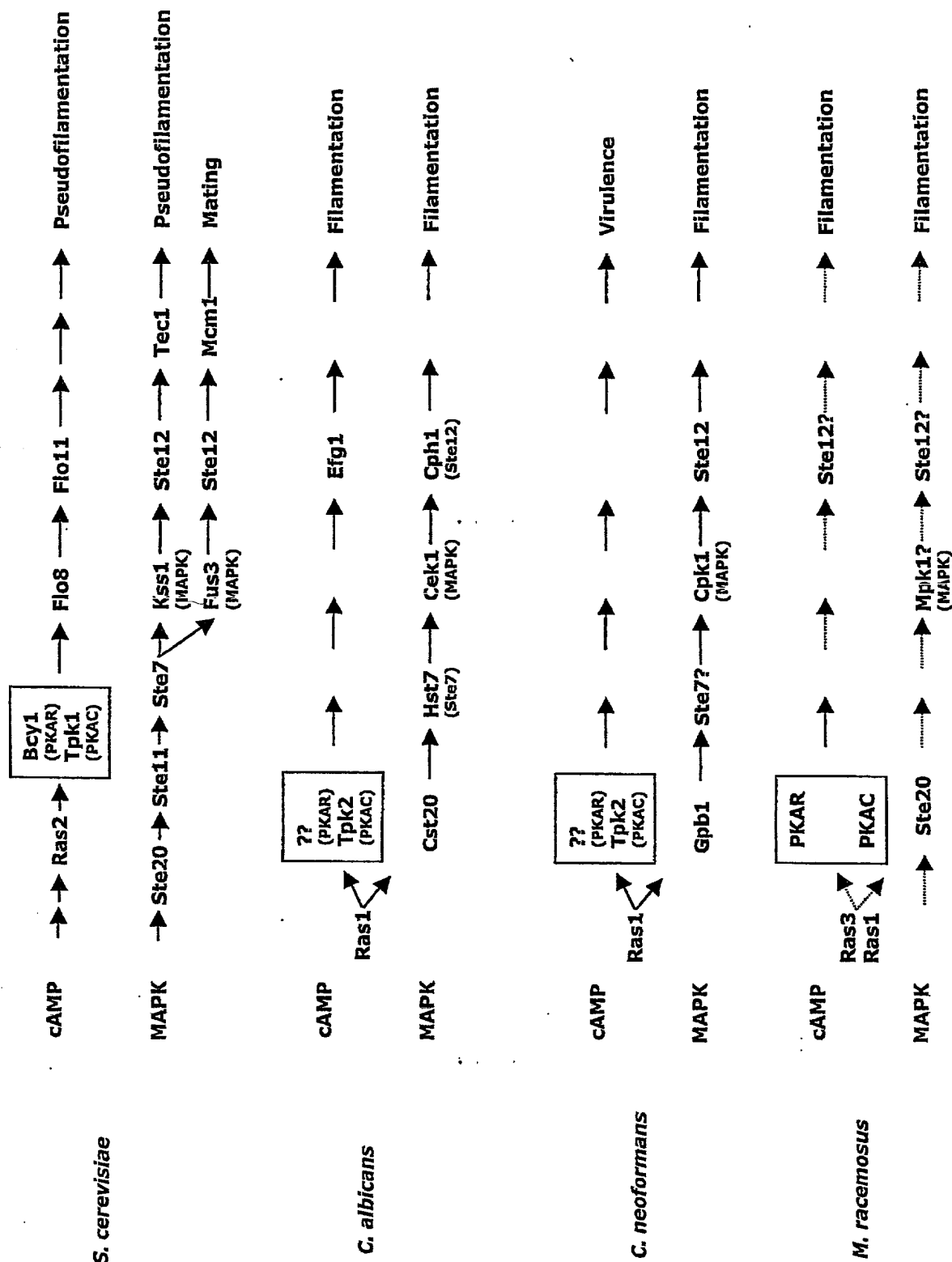


Fig. 2

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Fig. 3

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1 MADYTIPSELEF-----TKDLSREVLHQPAILVQFCHVFAKILACQKVMDSADPATKATIA-----B Beme
1 MSN-----HQQFISDELSQIQHEIISKNEQDVLFQCANFYFNKIQCAQSELSWSQQAERAGIDLFPSPVDHVNVS Calb
1 VSS-----LPKE-SQNELQLEONEINRANPSDLOHSANYFNRLKLEQRAFLKAREPEFKAKNIVLFPPEESFSRP Scer
1 MS-----FEEVYREIKALVDEONHSQVLOQCYDFEGEKIMKEE-----SVFRHEDT-----I Spom
1 M-----M-----Mrou

68 INDTSNDLHPLCEQOEDESQQQ-----GIQWETTHMGHPNDHGALHDDDDHIE Mcir
51 AASSSTG-----SPHGGGSVGENS-----PIRFRNSPFDNGBREBDEEGAO Anig
63 IZGEADDAEAARANSYAYSTD-----GR-----CTEDDDDDU Beme
73 SGVETVNDROHS--FKSPFQVNDPHSNHDEDPHAKDTKTDTAAAVGGGIFKSNEDVKKSASNPPTEKVDLPDPSPSSS Calb
72 QSACQSRSSRSMFKSPFVNDPHSN-----VFKSGENL-----PHEQDTH Scer
48 IESRSDG-----DES-----DELSELNDMVAGPEALGPAKVVPRG Spom
2 -----Mrou

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115 QQAQEEQHTREKTSTPPIEMHMAQRTSVSGETHQNNM--DDWTEDHYKENSEQOORLEKSTANFLRNLDEQY Scer
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2 -----DEEHY Mrou

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7 QIVUNAMTEKVR-KGATITIKQAGVGDYFYVVASGTFDQILKKQORP--L-----KVTSYERGGGSFGEALALMYNAP Mrou

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314 ENFYILIESGDEHVIDENGEEHFRHUKGNVYFGEALALNDKPRVATINAKGRLKQAKLGKKAFTRLIGPVLDTLKRN Beme
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403 -----EYRSNVPVA Anig
394 -----QDYKXVGEH Beme
449 PTK-----SQDPTAGH Calb
412 PTR-----H Scer
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Fig. 4

Fig. 5

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Fig. 6a

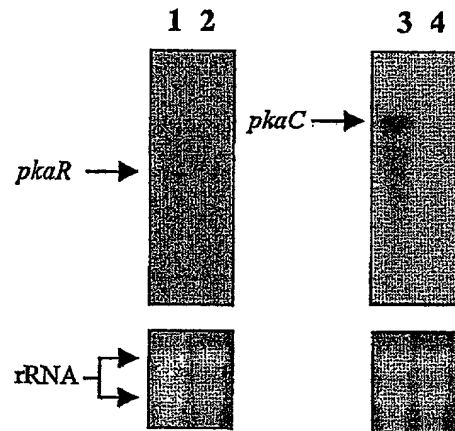


Fig. 6b

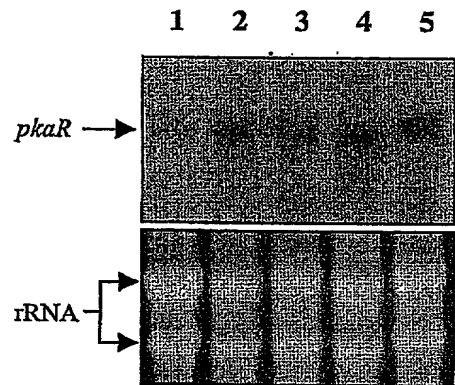
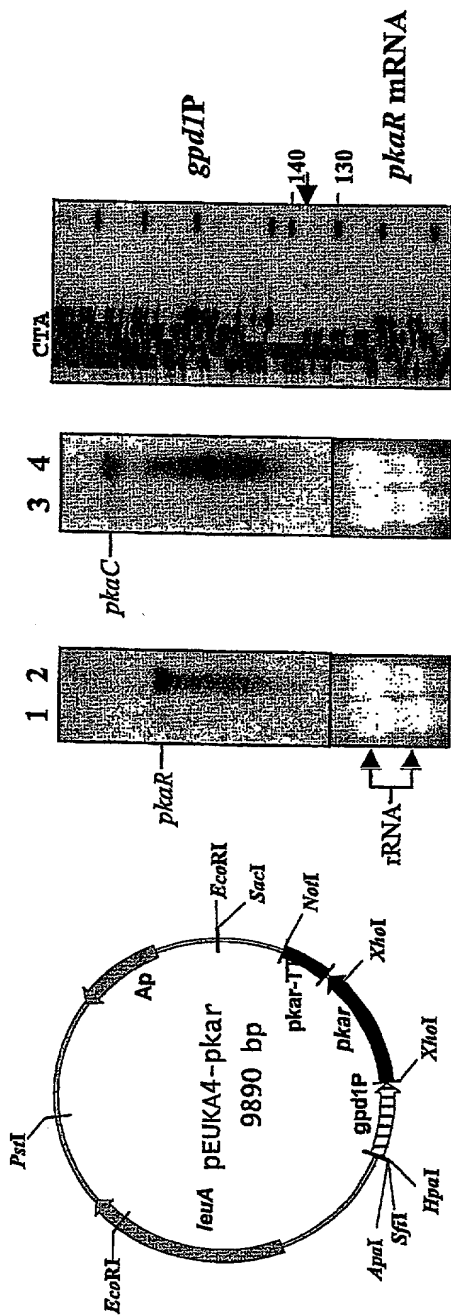


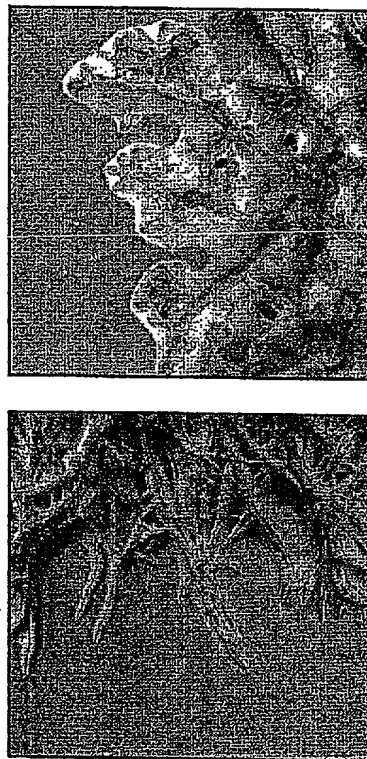
Fig. 7a



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XhoI

Fig. 7b



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200000 24626000

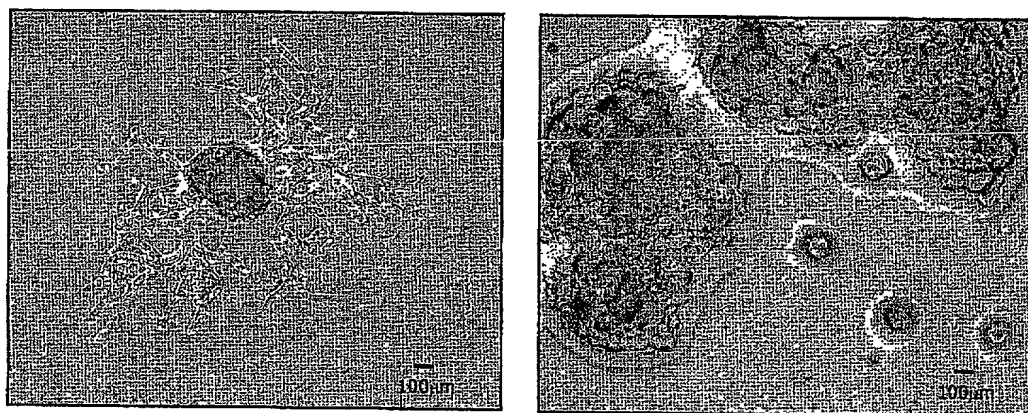


Fig. 8

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Fig. 9a

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31	KFFLATAPANWQENQVIRRYVI-----NHDEGFVSCVWNNLYFITGTDIVRCIVKHEHFGKTIIDRKK	Calb
38	KFFLATAPANWQENQVIRRYVI-----SNDEGFVSCVFNNLYITGTDIVRCIAYRMKFGREIVRKK	Klac
43	KYFTLSAIVDWQPTQIRRTLP-----TGDIYSCVWNNLYFITGTDIVRCIAERFOAFGRFVKNKK	Anid
19	KFFLATAPANWQENQVIRRYVI-----ANDEGFVSCVFNNLYFITGTDIVRCIYKRFHFGHTITDRKK	Cpur
81	EEGIFSDLRLNLKQHDALEEPKSELDMLYKNNCLRTQKKQKVF	Mcir
110	EEGIFSDLRLNLKCGIDATLEPKSEFISFIENMCLRTQKKQKVF	Scer
97	EEGIFSDLRLNLKCGIDATLEEPHSEFISFLEKNSCLRTQKKQKVF	Calb
104	EEGIFSDLRLNLKCGIDATLEPKSDLAFLYKNNCLRTQKKQKVF	Klac
108	EEGIFSDLRLNLKAGTIDATLEEPKSEFLDFLYKNNCLRTQKKQKVF	Anid
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Fig. 9b

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105	VLYEELMEDLNEQIKSGOPLDAHFQSFYQICGLKYTHSANVLRDLKPGNLLVNA	SLT2
145	VITCELMEDLHRVIRIQLSDHQCQPIYQILKALNAHSANVLRDLKPGNLLVNA	ERR1
101	ETM	MPK1
198	ETM	SPM1
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195	ETM	FMK1
202	ETM	SLT2
240	ETM	ERR1

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R F D G S V E A K D G K L V V N G H A I
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V V E S T G intron1
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Fig. 10

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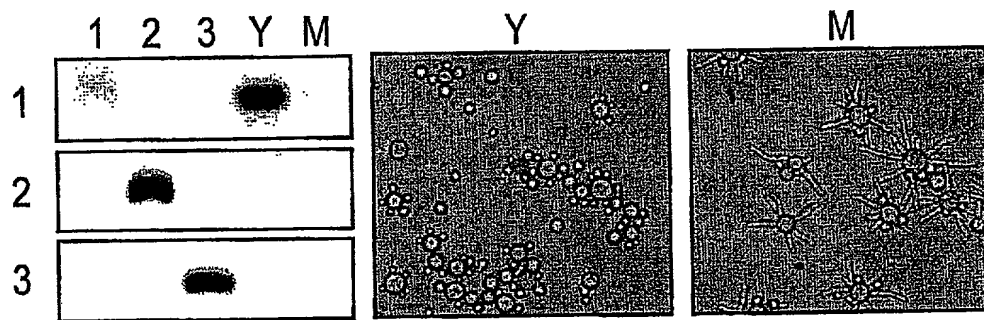


Fig. 11

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Fig. 12a

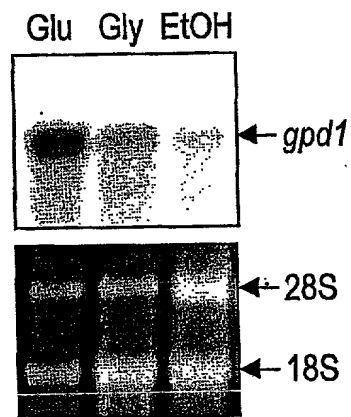
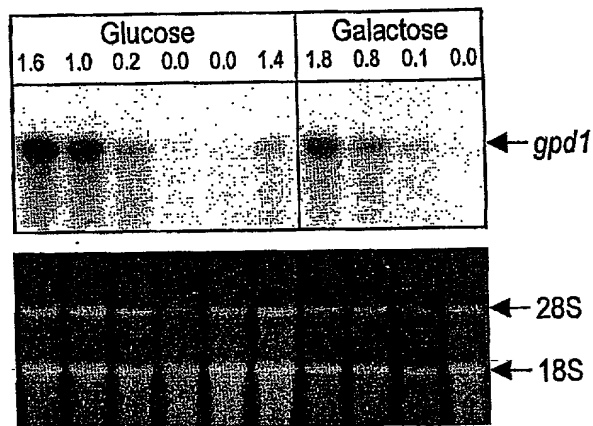


Fig. 12b



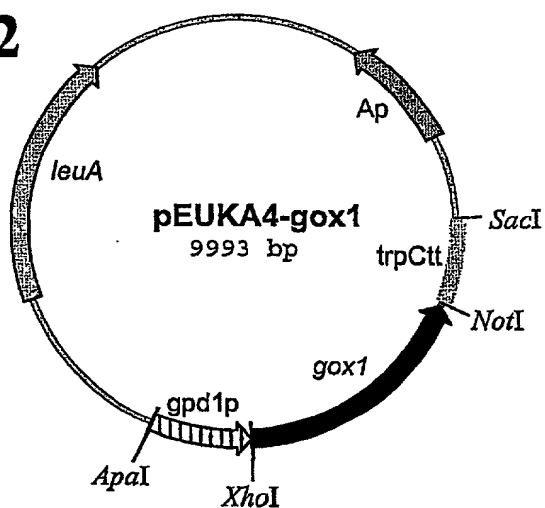
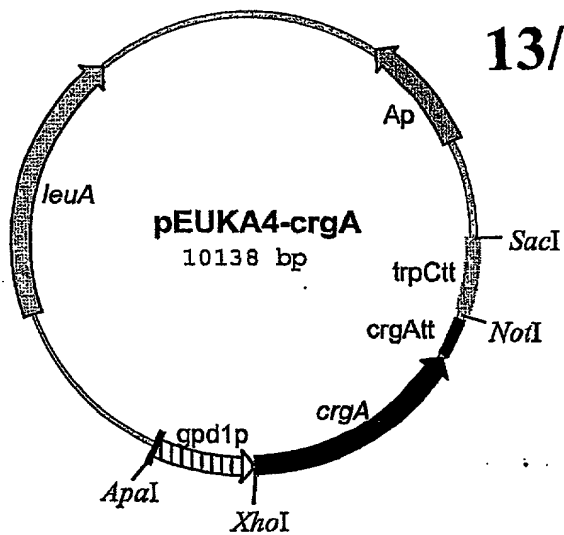


Fig. 13a

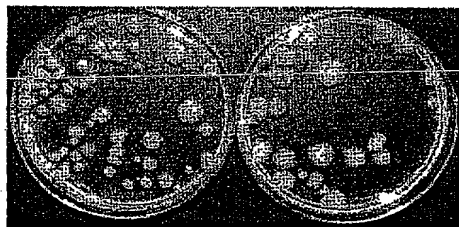


Fig. 13b



Fig. 13c

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Fig. 14a

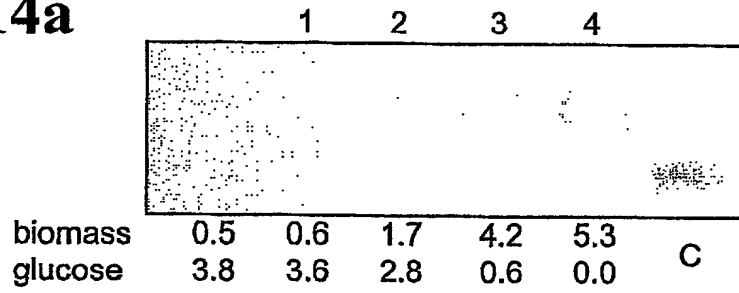


Fig. 14b

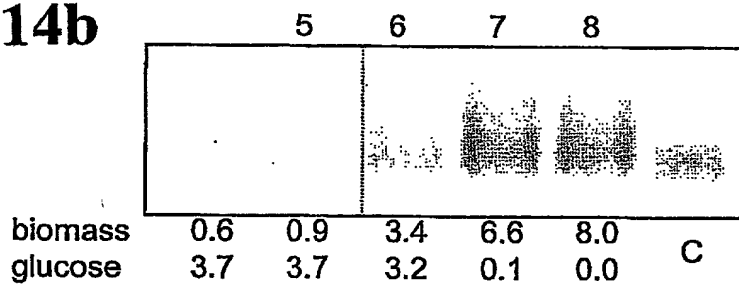


Fig. 14c

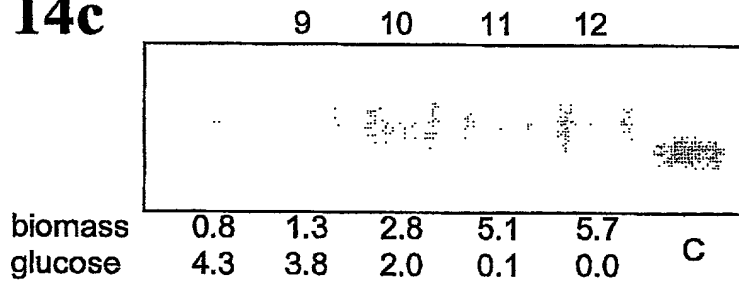


Fig. 14d

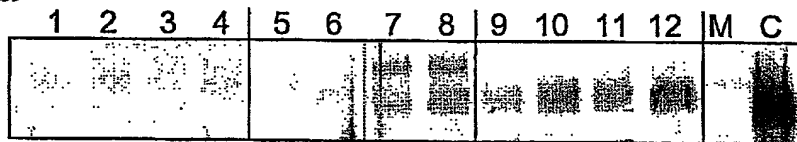


Fig. 14

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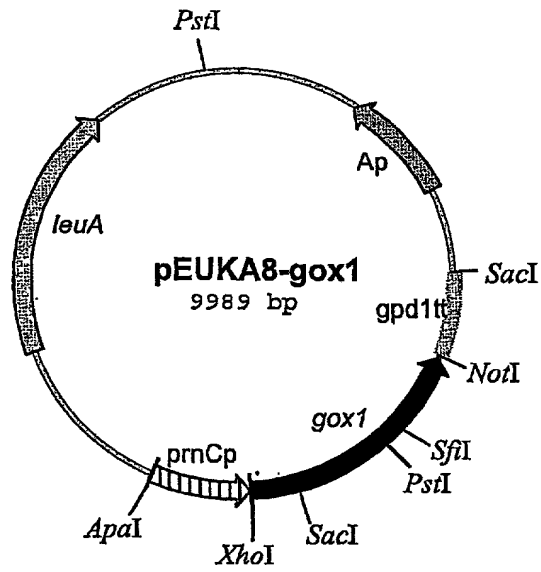


Fig. 15

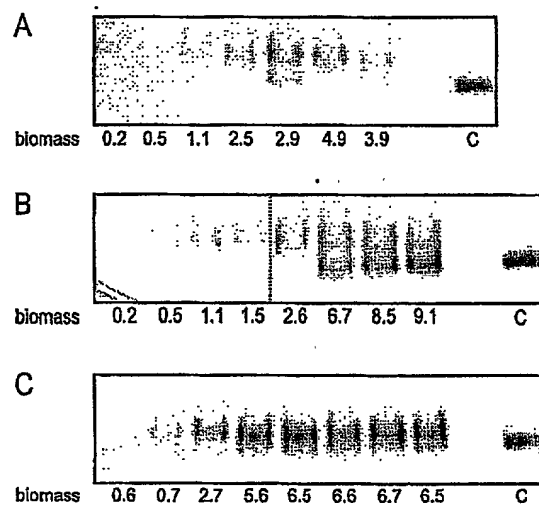


Fig. 16

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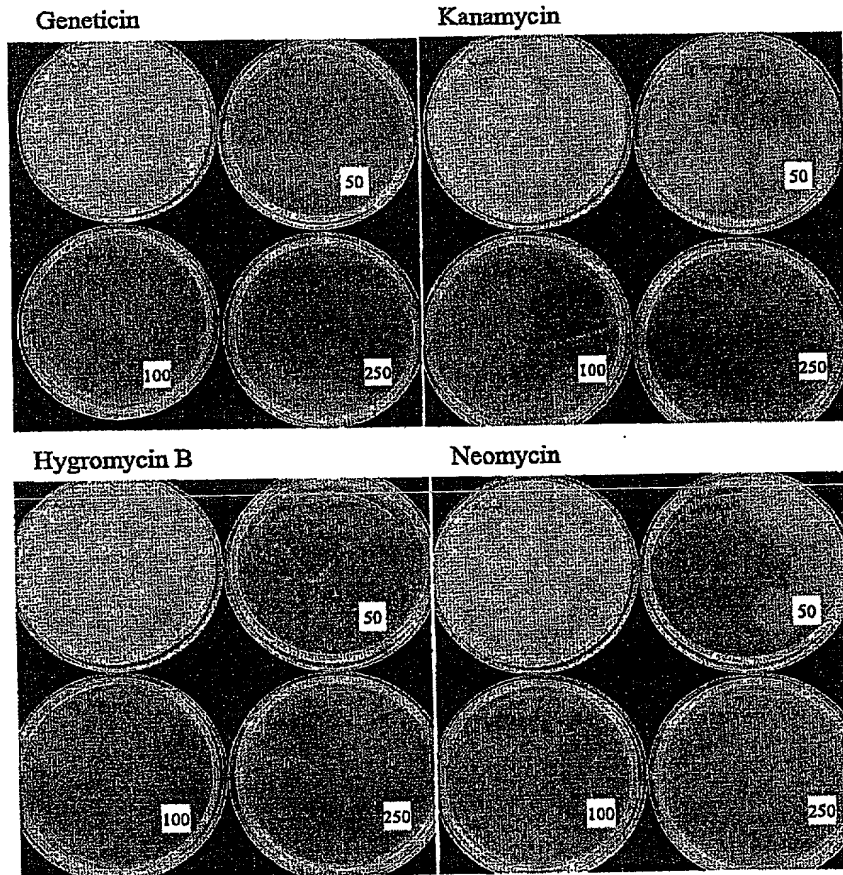


Fig. 17

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Fig. 18a

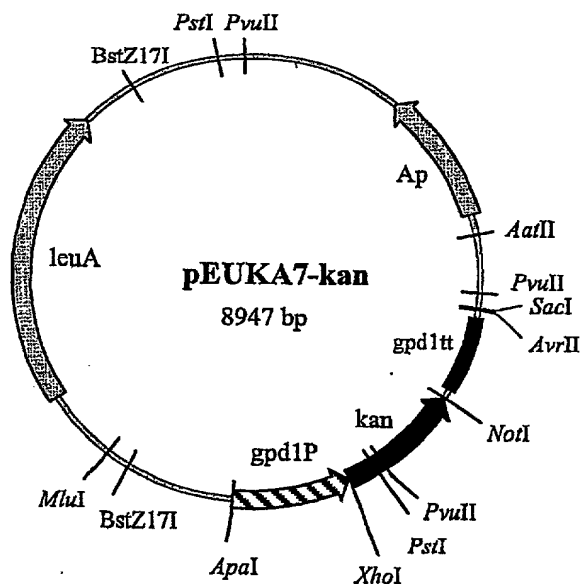


Fig. 18b

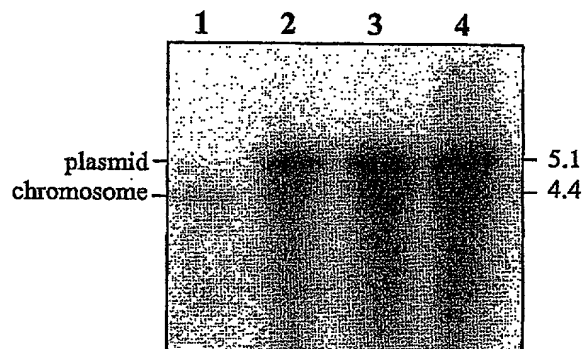
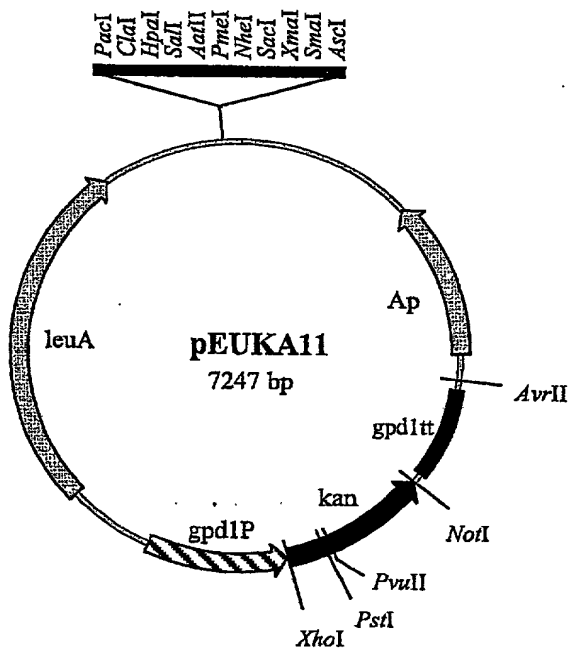


Fig. 18c



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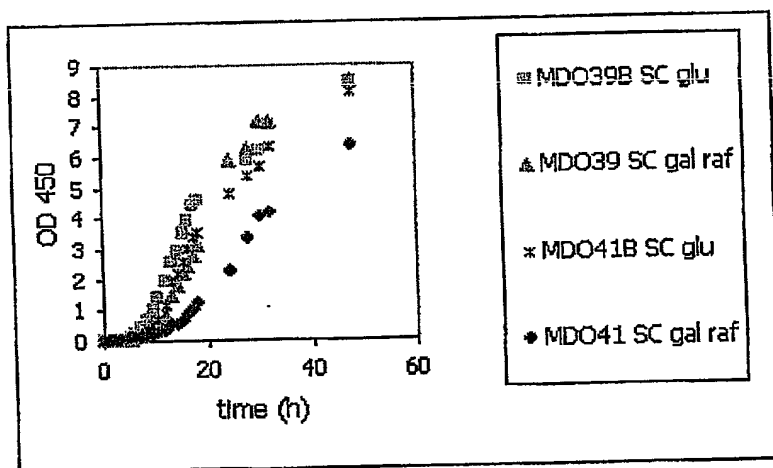


Fig. 19

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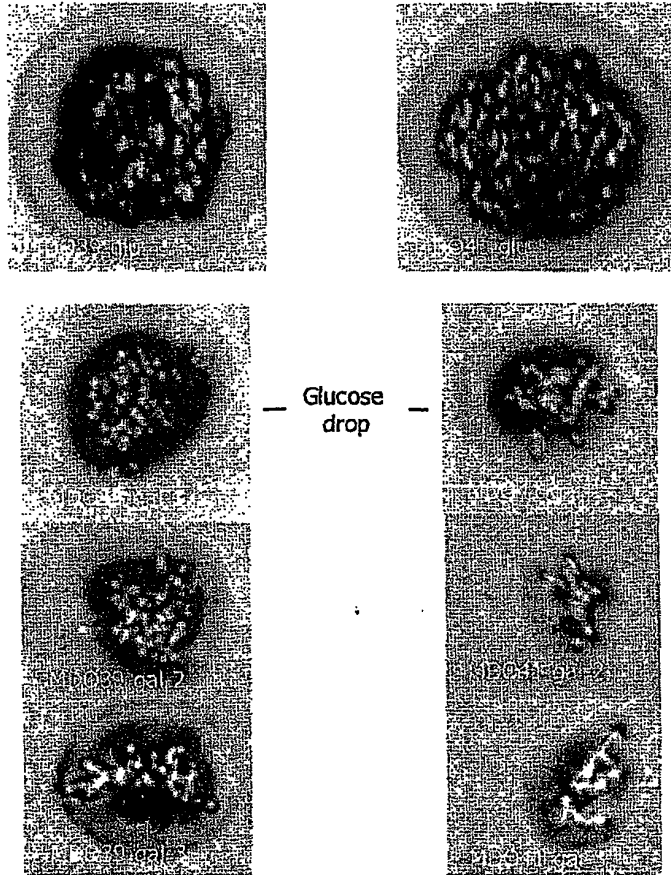


Fig. 20

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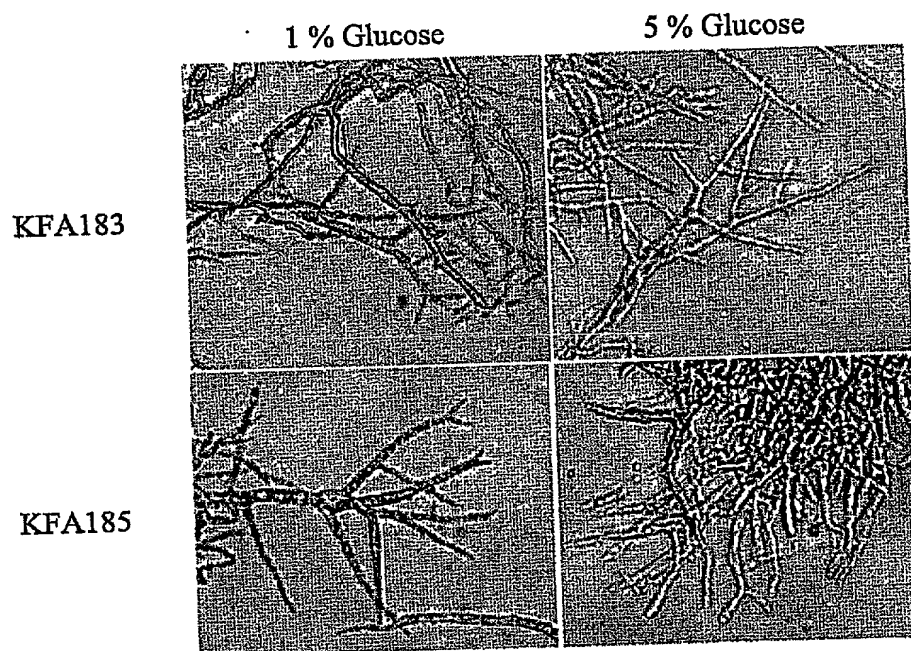


Fig. 21

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1 2

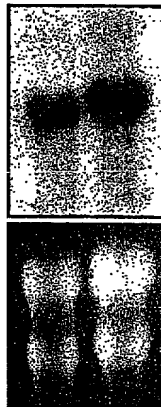


Fig. 22

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1 2 3 4 5

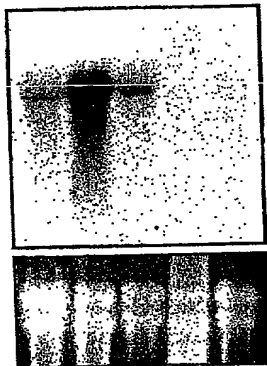


Fig. 23